

sequences, SEQ ID NOs:1-38, in computer readable form, and a paper copy of the sequence information which has been printed from the floppy disk.

The information contained in the computer readable disk was prepared through the use of the software program "PatentIn" and is identical to that of the paper copy.

This amendment contains no new matter. The amendments to the specification and claims introducing sequence ID numbers simply provide appropriate cross-reference from the sequences in the application to the formal sequence listing. Replacement Figures 5 and 6 also introduce no new matter. The letters that are now visible in the "POINTED/A-REGION" and the "ETS-DNA Binding Domain" can be determined by reference to Figure 4 and to SEQ ID NO 15 as filed. The corrections to the mESX sequence in Figures 5 and 6 can be determined by reference to the mESX sequence in the Sequence Listing as filed. Moreover, it is noted that the specification teaches that Applicants isolated and sequenced the human and mouse ESX genes. The corrections to Figures 5 and 6 simply reflect the correct polypeptide sequence and as such, are inherent in the isolated nucleic acids (*see, e.g., Kennecott Corp. v Kyocera Internat., Inc. and Kyoto Ceramic Co., Ltd.* 5 USPQ2d 1194 (Fed. Cir. 1987))

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at (415) 576-0200.







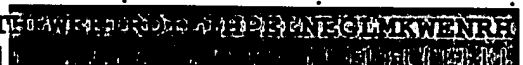
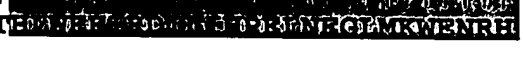

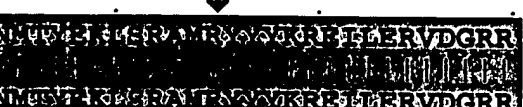

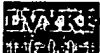

Respectfully submitted,



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ESX Primary Structure and Domain Homologies.

| | | | |
|--|-----|---|-----|
| mESX | 1 | MAATCEISNVFSNYFNAMYSSDPTLAPAPP.TTFGTEDLVLTLLNNQOMT | 49 |
| hESX | 1 | MAATCEISNIFSNYFSAMYSSDSTLASVPPAATFGADDLVLTLSNPQMS | 50 |
| E_2/E_3  | | | |
| mESX | 50 | LEGPEKASWTSERPQFWSKTQVLEWISYQVEKNKYDASSIDFSRCNMDGA | 99 |
| hESX | 51 | LEGTEKASWLGEQPQFWSKTQVLDWISYQVEKNKYDASAIDFSRCDMDGA | 100 |
| E_3/E_4  | | | |
| mESX | 100 | TLCSCALEELRLVFGPLGDQLHAQLRDLTSNSSDELSWIIELLEKDGMSF | 149 |
| hESX | 101 | TLCNCALEELRLVFGPLGDQLHAQLRDLTSSSSDELSWIIELLEKDGMAF | 150 |
| E_4/E_5 E_5/E_6   | | | |
| mESX | 150 | QESLGDLGPFSDQGSPPFAQELLDDGRQASPYCSTYGPAGSPGSSDVSTA | 199 |
| hESX | 151 | QEAL.DPGPFDQGSPPFAQELLDDGQQASPYHPSGCGAGAPSPGSSDVSTA | 199 |
| E_6/E_7  | | | |
| mESX | 200 | GTATPQSSHASDSGGSDVDLDLTESKVFPRDDFTDYKKGEPKHGKRKRGR | 249 |
| hESX | 200 | GTGASRSSHSSDSGGSDVDLDPTDGKLFPSDGFRDCKKGDPKHGKRKRGR | 249 |
| E_7/E_8  | | | |
| mESX | 250 | PRKLSKEYWDCLEGKKS KHAPRGTE  ENEGALMKWENRH | 299 |
| hESX | 250 | PRKLSKEYWDCLEGKKS KHAPRGTE  ENEGALMKWENRH | 299 |
| E_8/E_9  | | | |
| mESX | 300 | EGVEKPRSEAVAGLVGCKKNS  FFERVDGRR | 349 |
| hESX | 300 | EGVEKPRSEAVAGLVGCKKNS  FFERVDGRR | 349 |
| mESX | 350 |  GKNSSGWKEEEVGESRN | 371 |
| hESX | 350 |  GKNSSGWKEEEVLQSRN | 371 |




- POINTED / A-Region
-  Serine-Rich Box
-  Nuclear Targeting Sequence
-  ETS-DNA Binding Domain

Fig.5

Fig. 6